

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a member selected from the group consisting of:
- (a) a polynucleotide having at least 80% sequence identity to the polynucleotide of SEQ ID NO: 1, wherein the % sequence identity is based on the entire coding region for each reference sequence and is calculated by the GAP algorithm under default parameters;
  - (b) a polynucleotide encoding the polypeptide of SEQ ID NO: 2;
  - (c) a polynucleotide amplified from a *Zea mays* nucleic acid library using primers which selectively hybridize, under stringent hybridization conditions, to loci within the polynucleotide of SEQ ID NO: 1;
  - (d) a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 0.1X SSC at 60°C, to the polynucleotide of SEQ ID NO: 1;
  - (e) the polynucleotide of SEQ ID NO: 1;
  - (f) a polynucleotide which is complementary to a polynucleotide of (a), (b), (c), (d), or (e); and
  - (g) a polynucleotide comprising at least 30 contiguous nucleotides from a polynucleotide of (a), (b), (c), (d), (e), or (f).
2. A recombinant expression cassette, comprising a member of claim 1 operably linked, in sense or anti-sense orientation, to a promoter.
3. A host cell comprising the recombinant expression cassette of claim 2.
4. A transgenic plant comprising a recombinant expression cassette of claim 2.
5. The transgenic plant of claim 4, wherein said plant is a monocot.
6. The transgenic plant of claim 4, wherein said plant is a dicot.

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7. The transgenic plant of claim 4, wherein said plant is selected from the group consisting of: maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, and millet.

8. A transgenic seed from the transgenic plant of claim 4.

9. A method of modulating the level of Rad50 in a plant, comprising:

- (a) introducing into a plant cell a recombinant expression cassette comprising a Rad50 polynucleotide of claim 1 operably linked to a promoter;
- (b) culturing the plant cell under plant cell growing conditions;
- (c) regenerating a whole plant which possesses the transformed genotype; and
- (d) inducing expression of said polynucleotide for a time sufficient to modulate the level of Rad50 in said plant.

10. The method of claim 9, wherein the plant is maize.

11. An isolated protein comprising a member selected from the group consisting of:

- (a) a polypeptide of at least 20 contiguous amino acids from the polypeptide of SEQ ID NO: 2;
- (b) the polypeptide of SEQ ID NO: 2;
- (c) a polypeptide having at least 80% sequence identity to, and having at least one linear epitope in common with, the polypeptide of SEQ ID NO: 2, wherein said sequence identity is determined using the GAP program under default parameters; and
- (d) at least one polypeptide encoded by a member of claim 1.

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